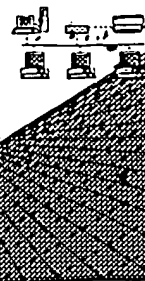


0590
08

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/920267
Source: OIPE
Date Processed by STIC: 08/09/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/920,267
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/920,267

TIME: 12:18:31

Input Set : A:\Cen249 Seq List 07-09-01.txt

Output Set: N:\CRF3\08092001\I920267.raw

4 <110> APPLICANT: Giles-Komar, Jill; Heavner, George; Snyder, Linda; Trikha, Mohit
 6 <120> TITLE OF INVENTION: DUAL INTEGRIN ANTIBODIES, COMPOSITIONS, METHODS AND USES
 8 <130> FILE REFERENCE: CEN 249
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/920,267
 C--> 10 <141> CURRENT FILING DATE: 2001-08-01
 10 <160> NUMBER OF SEQ ID NOS: 17
 12 <170> SOFTWARE: PatentIn Ver 2.0

pp 1-2,4
 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 5
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Homo sapiens
 W--> 19 <400> SEQUENCE: 1
 20 Arg Tyr Thr Met His

E--> 21
 31 <210> SEQ ID NO: 3
 32 <211> LENGTH: 10
 33 <212> TYPE: PRT
 34 <213> ORGANISM: Homo sapiens

W--> 35 <400> SEQUENCE: 3
 36 Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile

E--> 37 1 5 10
 39 <210> SEQ ID NO: 4
 40 <211> LENGTH: 10
 41 <212> TYPE: PRT
 42 <213> ORGANISM: Homo sapiens

W--> 43 <400> SEQUENCE: 4
 44 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala

E--> 45 1 5 10
 47 <210> SEQ ID NO: 5
 48 <211> LENGTH: 6
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens

W--> 51 <400> SEQUENCE: 5
 52 Asp Ala Ser Asn Arg Ala Thr

E--> 53 1 5
 55 <210> SEQ ID NO: 6
 56 <211> LENGTH: 7
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Homo sapiens

W--> 59 <400> SEQUENCE: 6
 60 Gln Gln Arg Ser Asn Trp Pro Pro

E--> 61 1 5
 347 <210> SEQ ID NO: 13

Does Not Comply
 Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/920,267

TIME: 12:18:31

Input Set : A:\Cen249 Seq List 07-09-01.txt

Output Set: N:\CRF3\08092001\I920267.raw

348 <211> LENGTH: 33
 349 <212> TYPE: DNA
 350 <213> ORGANISM: Homo sapiens
 W--> 351 <400> SEQUENCE: 13
 E--> 352 ctctcctgca gggccagtca gagtgttagc agctacttag(cc)
 525 <210> SEQ ID NO: 17
 526 <211> LENGTH: 799
 527 <212> TYPE: PRT
 528 <213> ORGANISM: Homo sapiens
 W--> 529 <400> SEQUENCE: 17

531 Met Pro Arg Ala Pro Ala Pro Leu Tyr Ala Cys Leu Leu Gly Leu Cys
 532 1 5 10 15
 534 Ala Leu Leu Pro Arg Leu Ala Gly Leu Asn Ile Cys Thr Ser Gly Ser
 535 20 25 30
 537 Ala Thr Ser Cys Glu Glu Cys Leu Ile His Pro Lys Cys Ala Trp
 538 35 40 45
 540 Cys Ser Lys Glu Asp Phe Gly Ser Pro Arg Ser Ile Thr Ser Arg Cys
 541 50 55 60
 543 Asp Leu Arg Ala Asn Leu Val Lys Asn Gly Cys Gly Gly Glu Ile Glu
 544 65 70 75 80
 546 Ser Pro Ala Ser Ser Phe His Val Leu Arg Ser Leu Pro Leu Ser Ser
 547 85 90 95
 549 Lys Gly Ser Gly Ser Ala Gly Trp Asp Val Ile Gln Met Thr Pro Gln
 550 100 105 110
 552 Glu Ile Ala Val Asn Leu Arg Pro Gly Asp Lys Thr Thr Phe Gln Leu
 553 115 120 125
 555 Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Leu Tyr Tyr Leu Met
 556 130 135 140
 558 Asp Leu Ser Leu Ser Met Lys Asp Asp Leu Asp Asn Ile Arg Ser Leu
 559 145 150 155 160
 561 Gly Thr Lys Leu Ala Glu Glu Met Arg Lys Leu Thr Ser Asn Phe Arg
 562 165 170 175
 564 Leu Gly Phe Gly Ser Phe Val Asp Lys Asp Ile Ser Pro Phe Ser Tyr
 565 180 185 190
 567 Thr Ala Pro Arg Tyr Gln Thr Asn Pro Cys Ile Gly Tyr Lys Leu Phe
 568 195 200 205
 570 Pro Asn Cys Val Pro Ser Phe Gly Phe Arg His Leu Leu Pro Leu Thr
 571 210 215 220
 573 Asp Arg Val Asp Ser Phe Asn Glu Glu Val Arg Lys Gln Arg Val Ser
 574 225 230 235 240
 576 Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Val Leu Gln Ala
 577 245 250 255
 579 Ala Val Cys Lys Glu Lys Ile Gly Trp Arg Lys Asp Ala Leu His Leu
 580 260 265 270
 582 Leu Val Phe Thr Thr Asp Asp Val Pro His Ile Ala Leu Asp Gly Lys
 583 275 280 285
 585 Leu Gly Gly Leu Val Gln Pro His Asp Gly Gln Cys His Leu Asn Glu
 586 290 295 300
 588 Ala Asn Glu Tyr Thr Ala Ser Asn Gln Met Asp Tyr Pro Ser Leu Ala

Errored: Field 211 indicated 33 nucleotide residues.
 The actual sequence listing contains 42
 nucleotide residues

33 42

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/920,267

TIME: 12:18:31

Input Set : A:\Cen249 Seq List 07-09-01.txt

Output Set: N:\CRF3\08092001\I920267.raw

```

589 305          310          315          320
591 Leu Leu Gly Glu Lys Leu Ala Glu Asn Asn Ile Asn Leu Ile Phe Ala
592          325          330          335
594 Val Thr Lys Asn His Tyr Met Leu Tyr Lys Asn Phe Thr Ala Leu Ile
595          340          345          350
597 Pro Gly Thr Thr Val Glu Ile Leu Asp Gly Asp Ser Lys Asn Ile Ile
598          355          360          365
600 Gln Leu Ile Ile Asn Ala Tyr Asn Ser Ile Arg Ser Lys Val Glu Leu
601          370          375          380
603 Ser Val Trp Asp Gln Pro Glu Asp Leu Asn Leu Phe Phe Thr Ala Thr
604 385          390          395          400
606 Cys Gln Asp Gly Val Ser Tyr Pro Gly Gln Arg Lys Cys Glu Gly Leu
607          405          410          415
609 Lys Ile Gly Asp Thr Ala Ser Phe Glu Val Ser Leu Glu Ala Arg Ser
610          420          425          430
612 Cys Pro Ser Arg His Thr Glu His Val Phe Ala Leu Arg Pro Val Gly
613          435          440          445
615 Phe Arg Asp Ser Leu Glu Val Gly Val Thr Tyr Asn Cys Thr Cys Gly
616          450          455          460
618 Cys Ser Val Gly Leu Glu Pro Asn Ser Ala Arg Cys Asn Gly Ser Gly
619 465          470          475          480
621 Thr Tyr Val Cys Gly Leu Cys Glu Cys Ser Pro Gly Tyr Leu Gly Thr
622          485          490          495
624 Arg Cys Glu Cys Gln Asp Gly Glu Asn Gln Ser Val Tyr Gln Asn Leu
625          500          505          510
627 Cys Arg Glu Ala Glu Gly Lys Pro Leu Cys Ser Gly Arg Gly Asp Cys
628          515          520          525
630 Ser Cys Asn Gln Cys Ser Cys Phe Glu Ser Glu Phe Gly Lys Ile Tyr
631          530          535          540
633 Gly Pro Phe Cys Glu Cys Asp Asn Phe Ser Cys Ala Arg Asn Lys Gly
634 545          550          555          560
636 Val Leu Cys Ser Gly His Gly Glu Cys His Cys Gly Glu Cys Lys Cys
637          565          570          575
639 His Ala Gly Tyr Ile Gly Asp Asn Cys Asn Cys Ser Thr Asp Ile Ser
640          580          585          590
642 Thr Cys Arg Gly Arg Asp Gly Gln Ile Cys Ser Glu Arg Gly His Cys
643          595          600          605
645 Leu Cys Gly Gln Cys Gln Cys Thr Glu Pro Gly Ala Phe Gly Glu Met
646          610          615          620
648 Cys Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Ser Thr Lys Arg Asp
649 625          630          635          640
651 Cys Val Glu Cys Pro Leu Leu His Ser Gly Lys Pro Asp Asn Gln Thr
652          645          650          655
654 Cys His Ser Leu Cys Arg Asp Glu Val Ile Thr Trp Val Asp Thr Ile
655          660          665          670
657 Val Lys Asp Asp Gln Glu Ala Val Leu Cys Phe Tyr Lys Thr Ala Lys
658          675          680          685
660 Asp Cys Val Met Met Phe Thr Tyr Val Glu Leu Pro Ser Gly Lys Ser
661          690          695          700

```

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/920,267

TIME: 12:18:31

Input Set : A:\Cen249 Seq List 07-09-01.txt

Output Set: N:\CRF3\08092001\I920267.raw

663 Asn Leu Thr Val Leu Arg Glu Pro Glu Cys Gly Asn Thr Pro Asn Ala
664 705 710 715 720
666 Met Thr Ile Leu Leu Ala Val Val Gly Ser Ile Leu Leu Val Gly Leu
667 725 730 735
669 Ala Leu Leu Ala Ile Trp Lys Leu Leu Val Thr Ile His Asp Arg Arg
670 740 745 750
672 Glu Phe Ala Lys Phe Gln Ser Glu Arg Ser Arg Ala Arg Tyr Glu Met
673 755 760 765
675 Ala Ser Asn Pro Leu Tyr Arg Lys Pro Ile Ser Thr His Thr Val Asp
676 770 775 780
678 Phe Thr Phe Asn Lys Phe Asn Lys Ser Tyr Asn Gly Thr Val Asp
679 785 790 795

E--> 682 1
E--> 684 13 *Delete*

VERIFICATION SUMMARY

DATE: 08/09/2001

PATENT APPLICATION: US/09/920,267

TIME: 12:18:32

Input Set : A:\Cen249 Seq List 07-09-01.txt

Output Set: N:\CRF3\08092001\I920267.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:283 W: Missing Blank Line separator, <400> field identifier
L:21 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:27 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:37 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:43 M:283 W: Missing Blank Line separator, <400> field identifier
L:45 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:45 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:11 SEQ:4
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:53 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:53 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:7 SEQ:5
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:61 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:61 M:252 E: No. of Seq. differs, <211>LENGTH:Input:7 Found:8 SEQ:6
L:67 M:283 W: Missing Blank Line separator, <400> field identifier
L:98 M:283 W: Missing Blank Line separator, <400> field identifier
L:125 M:283 W: Missing Blank Line separator, <400> field identifier
L:330 M:283 W: Missing Blank Line separator, <400> field identifier
L:337 M:283 W: Missing Blank Line separator, <400> field identifier
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:351 M:283 W: Missing Blank Line separator, <400> field identifier
L:352 M:254 E: No. of Bases conflict, LENGTH:Input:33 Counted:42 SEQ:13
L:352 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:42 SEQ:13
L:358 M:283 W: Missing Blank Line separator, <400> field identifier
L:365 M:283 W: Missing Blank Line separator, <400> field identifier
L:373 M:283 W: Missing Blank Line separator, <400> field identifier
L:529 M:283 W: Missing Blank Line separator, <400> field identifier
L:682 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17